

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph bridging from page 15, line 19 through page 16, line 18, with the following paragraph:

On the other hand, as a wild strain of *Aspergillus* genera, a strain in which the sequence of the SRE is CGGTCTTTTGTCGG (SEQ ID NO. 39) (α -glucosidase of *Aspergillus nidulans*) and a strain in which the sequence of the SRE has a CGGCGAATTCACGG (SEQ ID NO: 40)(glucoamylase of *Aspergillus oryzae*) are known. Furthermore, it has not been reported that in these wild strains, a decrease of promoter activity is not reported. When these sequences are compared with the SRE existing in the promoter in a Taka-amylase gene of *Aspergillus oryzae*, bases in the positions of 4th, 5th, 7th, 10th and 11th from the 5'-end side are not common to each other. Consequently, it is thought that these bases have a low level of contribution to the enhancer function of the SRE. That is to say, it is thought that even if these bases are substituted by others, the enhancer function of the SRE may be maintained with high probability. Specifically, even if the base in the 4th position from the 5'-end side is T or C; the base in the 5th position from the 5'-end side is C or G; the base in the 7th position from the 5'-end side is A; the base in the 10th position from the 5'-end side is G or C; and the base in the 11th position from the 5'-end side is T, the enhancer function is expected to be maintained. However, when the binding property due to the structure of the individual structure is considered, it is thought to be desirable that the bases in the 6th to 9th and 11th positions from the 5'-end side, and further preferably the bases in the 4th to 11th positions from the 5'-end side is A or T.